VL D I Q M T Q T T S S L S A S L G D R V T gatatccagatgacccagactacatcctcctgtctgcctctctgggagacagagtcacc I S C R A S Q D I S N Y L N W Y Q Q K P attagttgcagggcaagtcaggacattagcaattattaaactggtatcagcagaaacca D G T V K L L I Y Y T S I L H S G V P S gatggaactgttaaactcctgatctactacacacaatattacactcaggagtcccatca R F S G S G S G T D Y S L T I S N L E Q aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaa E D F A T Y F C Q Q G N T L P W T F G G gaagattttgccacttacttttgccaacaggttaatacgcttccgtggacgttcggtgg G T K L E I K ggcaccaagctggaaatcaa

VH

FIG. 1

## Nucleotide/residue numbering shown first followed by Kabat Numbering

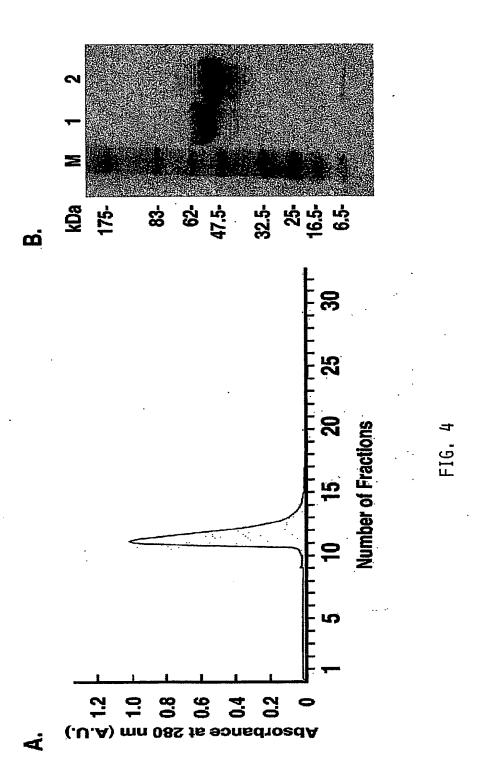
1	0	49	42 gga GLY G		
2	1 gat ASP D	50	43 act THR T	85	78 ctg LEU L
3	2 atc ILE I	51	44 gtt VAL V	86	79 gag GLU E
4	3 cag GLN Q	<b>52</b>	45 aaa LYS K	87	80 caa GLN Q
5	4 atg MBT M	52 53	46 ctc LEU L	88	81 gaa GLU E
6	5 acc THR T		47 ctg LEU L	89	82 gat ASP D
7	6 cag GLN Q	. <b>54</b>	48 atc ILE I	90	83 ttt PHE F
8	7 act THR T	55 56	49 tac TYR Y	91	84 gcc ALA A
9	8 aca THR T	56	50 tac TYR Y	92	85 act THR T
10	9 tcc SER S	57 58	51 aca THR T	93	86 tac TYR Y
11	10 tcc SER S		52 tca SBR S	94	87 ttt PHE P
12	11 ctg LEU L	59 60	53 ata ILE I	95	88 tgc CYS C
13	12 tct SER S	61	54 tta LEU L	96	89 caa GLN Q
14	13 gcc ALA A	62 <sup>.</sup>	55 cac HIS H	97	90 cag GLN Q
15	14 tet SER S	63	56 tca SER S	98	91 ggt GLY G
16	15 ctg LEU L	64	57 gga GLY G	99	92 aat ASN N
	,		58 gtc VAL V	100	93 acg THR T
		65 66	59 cca PRO P	101	94 ctt LEU L
17	16 gga GLY G	<b>67</b>	60 tca SER S	102	95 ccg PRO P
18	17 gac ASP D	<b>68</b>	61 agg ARG R	103	95A
19	18 aga ARG R	69	62 ttc PHE F	104	95B
20	19 gtc VAL V	70	63 agt SER S	105	95C
21	20 acc THR T	71	64 ggc GLY G	106 <sup>.</sup>	95D
22	21 att ILE I	72	65 agt SER S	107	95E
23	22 agt SER S	73	66 ggg GLY G	108	957
24	23 tgc CYS C	74	67 tct SER S	109	
25	24 agg ARG R	75	68 gga GLY G	110	97 acg THR T
26	25 gca ALA A	76	69 aca THR T	111	98 ttc PHE F
27	26 agt SER S	77	70 gat ASP D	112	99 ggt GLY G
28	27 cag GLN Q	78	71 tat TYR Y	113	100 gga GLY G
29	27A	79	72 tct SER S	114	101 ggc GLY G
30	27B	80	73 ctc LEU L	115	102 acc THR T
31	27C 27D	81	74 acc THR T	116	103 aag LYS K
32	27B	82	75 att ILB I	117	104 ctg LEU L
33	27F	83	76 agc SER S	118	105 gaa GLU E
34	28 gac ASP D	84	77 aac ASN N	119	106 atc ILE I
35	29 att ILE I	-		120	106A
36	30 age SER S		•	121	107 aaa LYS K
37	31 aat ASN N		•	122	108
38	32 tat TYR Y			. 123	109 •
39	33 tta LEU L				
40 41	34 aac ASN N		•		
41	35 tgg TRP W				
42	36 tat TYR Y				
44	37 cag GLN Q				
45	38 cag GLN Q				
46	39 aaa LYS K				
47	40 cca PRO P				
48	41 gat ASP D				
7.0	3	-			

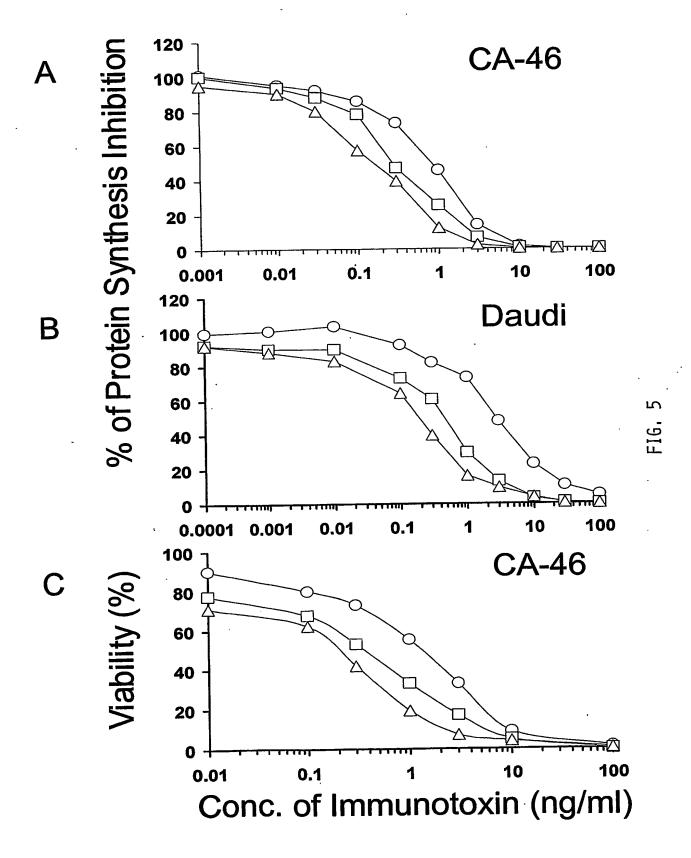
FIG. 2

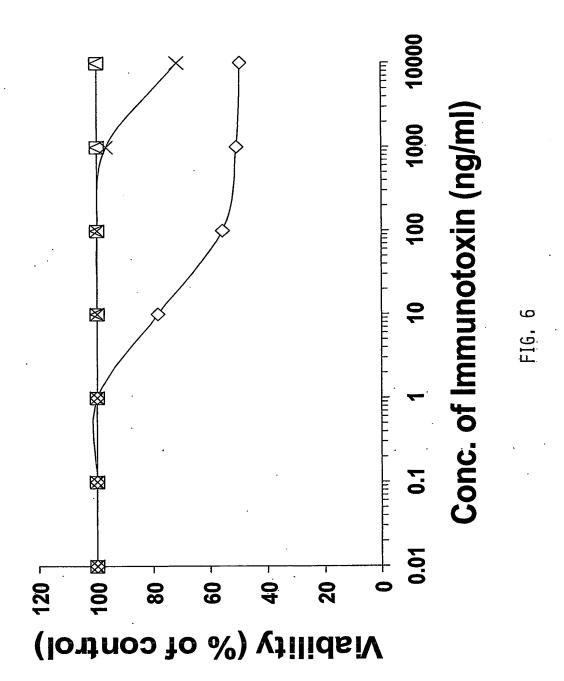
## Nucleotide/residue numbering shown first followed by Kabat Numbering

				•	
_	•	49	46 gag GLU B	05	70 has mun v
1	0	50	47 tgg TRP W	85 85	79 tac TYR Y
2	1 gaa GLU E	51	48 gtc VAL V	86	80 ctg LEU L
3	2 gtg VAL V	52	49 gca ALA A	87	81 caa GLN Q
4	3 cag GLN Q	53	50 tac TYR Y	88	82 atg MET M
5	4 ctg LEU L	54,	51 att ILB I	89	82A agc SER S
6	5 gtg VAL V	55	52 agt SBR S	90	82B agt SER S
7	6 gag GLU E	56	52A agt SER S	91	82C ctg LEU L
8	7 tot SER S	57	52B	92	83 aag LYS K
9	8 ggg GLY G	58	52C	93	84 tot SER S
10	9 gga GLY G	59	53 ggt GLY G	94	85 gag GLU E
11	10 ggc GLY G	60	54 ggt GLY G	95	86 gac ASP D
12	11 tta LEU L	61	55 ggt GLY G	96	87 aca THR T
13	12 gtg VAL V	62	56 acc THR T	97	88 gcc ALA A
14	13 aag LYS K	63	57 acc THR T	98	89 atg MET M
15	14 cct PRO P	64	58 tac TYR Y	99	90 tat TYR Y
16	15 gga GLY G	65	59 tat TYR Y	100	
17	16 ggg GLY G	66	60 cca PRO P	101	92 tgt CYS C
18	17 tcc SER S	67	61 gac ASP D	102	
19	18 ctg LEU L	68	62 act THR T	103	94 aga ARG R
20	19 aaa LYS K	69	63 gtg VAL V	104	95 cat HIS H
20 21	20 ctc LEU L	70	64 aag LYS K	105	96 agt SER S
22	21 tec SER S	71	65 ggc GLY G	106	97 ggc GLY G
23	22 tgt CYS C	72	66 cga ARG R	107	98 tac TYR Y
24	23 gca ALA A	<b>`73</b>	67 ttc PHE F	108	99 ggt GLY G
25 25	24 gcc ALA A	74	68 acc THR T	109	100 agt SER S
26	25 tct SER S	75	69 atc ILE I	110	100A agc SER S
20 27	26 gga GLY G	76	70 tcc SER S	111	100B tac TYR Y
28	27 ttc PHE F	77	71 aga ARG R	112	100C ggg GLY G
<b>2</b> 9	28 gct ALA A	78	72 gac ASP D	113	100D gtt VAL V
30	29 ttc PHE F	79	73 aat ASN N	114	100E ttg LEU L
31	30 agt SER S	80	74 gcc ALA A	115	100F
32	31 atc ILE I	81	75 aag LYS K	116	100G
33	32 tat TYR Y	82	76 aac ASN N	117	100H
34	33 gac ASP D	83	77 acc THR T	118	100I
35	34 atg MET M	84	78 ctg LEU L	119	100J
36	35 tet SER S			120	100K ttt PHE P
30 37	35A			121	101 gct ALA A
38	35B			122	102 tac TYR Y
39	36 tgg TRP W			123	103 tgg TRP W
40	37 gtt VAL V			124	104 ggc GLY G
41	38 cgc ARG R			125	105 caa GLN Q
42.	39 cag GLN Q			126	106 ggg GLY G
43	40 act THR T			127	107 act THR T
44	41 ccg PRO P			128	108 ctg LEU L
45	42 gag GLU E			129	109 gtc VAL V
46	43 aag LYS K			130	110 act THR T
47	44 agg ARG R			131	111 gtc VAL V
48	45 ctg LEU L			132	112 tet SER S
40	+-3			133	113 gca ALA A

FIG. 3







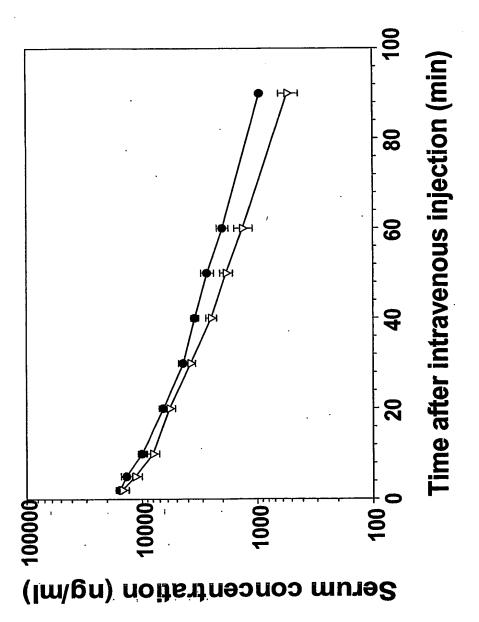


FIG. 7

